

RESULT 2
 ABK92167
 ID ABK92167 standard; DNA; 3810 BP.
 XX
 AC ABK92167;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 XX
 OS Mammalia.
 XX
 PN W0200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US032045.
 XX
 PR 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 26-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezl P;
 XX
 DR WPI; 2002-471335/50.
 DR P-PSDB; ABG61852.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 339-340; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences
 XX
 SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.1 0 Length: 3810
 Score: 1123.00 Matches: 1123
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: 6 Gaps: 0

US-10-643-795A-123 (1-1127) x ABK92167 (1-3810)

Qy 5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24

Db 3 ACGGAGAAAGCCACCGATGCCTACGGAGAGCTGGACTTCAAGGGGGGCGCGCAAGAC 62
 Qy 25 SerAsnPheLeuArgLeuSerAspArgThrAspProAlaAlaValTyrSerLeuValThr 44
 Db 63 AGCAATTTCCTCGCGCTCTCTGACCGAAGCGATCCAGCTGCAGTTTATAGTCTGGTCACA 122
 Qy 45 ArgThrTrpGlyPheArgAlaProAsnLeuValValSerValLeuGlyGlySerGlyGly 64
 Db 123 CGCACATGGGGCTTCGGTCCCCGAACCTGGTGGTGTGTCAGTGTGGGGGATGGGGGGGC 182
 Qy 65 ProValLeuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln 84
 Db 183 CCGGTCTCTCAGACCTGGCTGCAGGACCTGCTGGTGTGGGCTGGTGGGGGCTGCCAG 242
 Qy 85 SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly 104
 Db 243 AGCACAGAGACCTGGATTGTCTGCTGGGGTCTGCACACGGGATCGGCGGCTATGTTGGT 302
 Qy 105 ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly 124
 Db 303 GTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGACCAAGGTGGTGCCATGGGT 362
 Qy 125 ValAlaProTrpGlyValValArgAsnArgAspThrLeuIleAsnProLysGlySerPhe 144
 Db 362 GTGGGGGCTGGGGTGGTGGGGAATAGAGACACCTCATCAACCCAGGGGCTGGTTC 422
 Qy 145 ProAlaArgTyrArgTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspTyr 164
 Db 423 OCTGOGAGGTACCGGTGGCGGGTGACCGGAGGACGGGGTCCAGTTTCCCTGGACTAC 482
 Qy 165 AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn 184
 Db 483 AACTACTCGGCTTCTCTGTTGGAGCAGCGGCACACAGGCTGCTGGGGGGGAGAAC 542
 Qy 185 ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnLysThrGlyValGlyGlyThr 204
 Db 543 CGCTTCGGCTTGGGCTGGAGTCTCATCTCACAGCAGAGACGGGCGTGGGAGGACT 602
 Qy 205 GlyIleAspIleProValLeuLeuLeuLeuIleAspGlyAspGluLysMetLeuThrArg 224
 Db 603 GGAATTGACATCCCTGCTGCTGCTCTGATGATGGTGATGAGAAAGATGTTGACCGGA 662
 Qy 225 IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla 244
 Db 663 ATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCTCTGGCTGGCTCAGGGGGAGCT 722
 Qy 245 AlaAspCysLeuAlaGluThrLeuGluAspThrLeuAlaProGlySerGlyGlyAlaArg 264
 Db 723 CGGGACTGCTTGGCGGAGACCTTGAAGACACTCTGGCCCCAGGAGTGGGGGAGCCAG 782
 Qy 265 GlnGlyGluAlaArgAspArgIleArgArgPhePheProLysGlyAspLeuGluValLeu 284
 Db 783 CAAGGCGAAGCCGAGATCGAATCAGGCGTTTCTTCCAAAGGGGACCTTGAGGTCCT 842
 Qy 285 GlnAlaGlnValGluArgIleMetThrArgLysGluLeuLeuThrValTyrSerSerGlu 304
 Db 843 CAGGCCAAGTGGAGAGGATTATGACCCGGAAGAGAGCTCCTGACAGTCTATCTCTCGAG 902
 Qy 305 AspGlySerGluGluPheGluThrIleValLeuLysAlaLeuValLysAlaCysGlySer 324
 Db 902 GATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCTGTGGAGAG 962
 Qy 325 SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp 344
 Db 963 TCGGAGGCTCAGGCTACCTGGATGAGCTGGTTTTGGCTGTGGCTTGGAAACGGGTGGAC 1022
 Qy 345 IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla 364
 Db 1023 ATTGCCAGAGTGAACCTCTTCGGGGGGACATCAATGGCGGTCTTCATCTCGAAGCT 1082
 Qy 365 SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis 384
 Db 1083 TCCCTCATGGAGCCCTGCTGAATGACCGGCTGAGTCTGTGGGCTTGTCTATTCCAC 1142
 Qy 385 GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla 404

Db 1143 |||||GGCCTCAGCCTGGGCGCACTTCTGACCCGATGCGCCTGGCCCACTCTACAGCGCGCG 1202
 Qy 405 ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyThrLys 424
 Db 1203 |||||CGCTCCAACTCGCTCATCCGCAACCTTTTGGACCAAGCGTCCACAGCGCAGGACCAAA 1262
 Qy 425 AlaProAlaLeuLysGlyGlyAlaAlaGluLeuArgProAspValGlyHisValLeu 444
 Db 1263 |||||GCCCAAGCCCTAAAGGGGAGCTGCGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTG 1322
 Qy 445 ArgMetLeuLeuGlyLysMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro 464
 Db 1323 AGGATGCTGCTGGGGAAGATGTGGCGCGGAGGTACCCCTCCGGGGGCGCTGGGACCT 1382
 Qy 465 HisProGlyGlnGlyPheGlyGluSerMetTyrLeuLeuSerAspLysAlaThrSerPro 484
 Db 1383 CACCCAGGCGCAGGCTTCGCGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCGG 1442
 Qy 485 LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuLeuTrpAlaLeu 504
 Db 1443 CTCTGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTCTTTGGGCACCT 1502
 Qy 505 LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer 524
 Db 1503 TTGCTGAACAGGCGACAGATGGCCATGTACTTCTGGGAGATGGGTTCACATGCAGTTCC 1562
 Qy 525 SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu 544
 Db 1563 TCAGCTCTTGGGGCGCTGTTGCTGCTCGGGGTATGGCACGCTGGAGCTGACGCTGAG 1622
 Qy 545 GluAlaAlaArgArgLysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe 564
 Db 1623 GAGGCAGCACGGAGGAAGACCTGGCGTTCAAGTTTGAAGGATGGCGGTTGACCTCTTT 1682
 Qy 565 GlyGluCysTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro 584
 Db 1683 GCGAGTGTCTATGCGCAGTGAAGTGAAGGCTGCGCGCTCTCTCTCGTGTGCTGCGCC 1742
 Qy 585 LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe 604
 Db 1743 GTCTGGGGGATGCCACTTGCTCCAGCTGGCCATGCAAGCTGAGGCGCGTGGCTCTTT 1802
 Qy 605 AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr 624
 Db 1803 GCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGTGGGAGATATGGCCAGCACT 1862
 Qy 625 ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProLeuIleTyrThrArgLeu 644
 Db 1863 ACACCATCTGGGCGCTGGTCTCGACTTCTTTTGGCTCCACCTCATCTACACCGGCTC 1922
 Qy 645 IleThrPheArgLysSerGluGluGluProThrArgGluGluLeuGluPheAspMetAsp 664
 Db 1923 ATCACTTCAGGAATCAGAAAGAGGAGCCACACGGAGGAGCTAGAGTTTACATGGAT 1982
 Qy 665 SerValIleAsnGlyGluGlyProValGlyThrAlaAspProAlaGluLysThrProLeu 684
 Db 1983 AGTGTCATTAAATGGGGAAGGGCTGTGCGGACGGCGAGCCACCGGAGAGAGACCGCGT 2042
 Qy 685 GlyValProArgGlnSerGlyArgProGlyCysGlyGlyGlyArgGlyArgGlyArg 704
 Db 2043 GGGGTCCCGCGCCAGTCGGGCCCTCGGGTGTCTGCGGGGCGCGCTCGGGGGCGCGG 2102
 Qy 705 CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal 724
 Db 2103 TGCTTACGCGCGTGGTTCCACTTCTGGGGGCGCGCGGTGACCATCTTCATGGGCAACGT 2162
 Qy 725 ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro 744
 Db 2163 GTACGCTACCTGCTGTCTTCTGCTGCTTTCTCGCGGGTGTCTGCTGTGGATTTCAGCGC 2222
 Qy 745 AlaProProGlySerLeuGluLeuLeuLeuTyrPheTrpAlaPheThrLeuLeuCysGlu 764
 Db 2223 GCGCGCGCGGCTCCCTGGAGCTGCTGCTGCTATTCTTGGGGTTTCAGGCTGCTGTGGAG 2282
 Qy 765 GluLeuArgGlnGlyLeuSerGlyGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro 784

Dy		2283	GAACTGGCCAGGCGCTGAAGGGAGCGGGGGACAGCTGCAGCAGGGGGGCCGGGGCT	2342
Db		785	GlyHisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerThrAsnGlnCys	804
Db		2343	GGCCATGCCTCACTGAGCGAGCGCTGGCGCTCTACTGTGCACCAGCTGGAACAGTCG	2402
Qy		805	AspLeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu	824
Db		2403	GACCTAGTAGCTCTCACTTGCTTCTCTCTGGCGTGGGCTGC CGCTGACCCGGGTTTG	2462
Qy		825	TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeu	844
Db		2463	TACCACCTGGGCGSACGTGCTCTGCAAGCATCTGATGTTTCAGGTCGGGTCGTT	2522
Qy		845	HisIlePheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetMet	864
Db		2523	CACA TCTT CACG GT CAACA A AC G TG GG GC CC AG AT G CT CAT G GT G AG CA AT GA TG	2582
Qy		865	LysAspValPhePhePheLeuPhePheLeuGlyValTrpLeuValAlaTyrGlyValAla	884
Db		2583	AAGSAGGTGTTCTCTTCCTCTTCTCTCTCGSGTGTGGCTGGTACGCTATGGCTGGCC	2642
Qy		885	ThrGluGlyLeuLeuArgProArgAaspSerAspPheProSerIleLeuArgArgValPhe	904
Db		2643	ACGSAAGGGCTCTGAGGCAACGGGACGTA GACTTCCAAGA TCTTGCGGCGGCTTTC	2702
Qy		905	TyrArgProTyrGlnLeuGlnIlePheGlyGlnLeuGlnLeuAspMetAspValAlaLeu	924
Db		2703	TACGTCCTCTACCTCGAGATCTTGGSCAGATTCCCAGSAGACATGSAGCTGGCCCTC	2762
Qy		925	MetGluHisSerAanCysSerSerGluProGlyPheThrAlaHisProProGlyAlaGln	944
Db		2763	ATGAGCACAGCAACTGCTGCTGGAGCGGCGCTTGGGCAACCCCTCTGGGCGCAG	2822
Qy		945	AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValValLeuLeuValIlePhe	964
Db		2823	GGGGCACTCGGCTCTCCAGATG GCCAACTGGCTGGTGGTGCTGCTCTCGTATCTTC	2882
Qy		965	LeuLeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPhe	984
Db		2893	CTGCTCGTGGCCAACTCTGCTGGTCAACTCTGCTCATTGCCATGTCAGTATACAACT	2942
Qy		995	GlyLysValGlnGlyYasnSerAspLeuTyrTrpLysAlaArgGluLeuLeuArgLeu	1004
Db		2943	GGCAAAGTACAGGGCAACAGCATCTCTACTGGAAGGCGAGCGTTACCGCTCATCCGG	3002
Qy		1005	GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeu	1024
Db		3003	GAATTCACTCTGGGCGCGGCTGGCCCCGGCTTTATGTCATCTCCCACTGCGGCTC	3062
Qy		1025	LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerProAlaLeuGlu	1044
Db		3063	CTGCTAGGCAATGTGCAGGCGACCCGAGSAGCCCCAGCGCTCTCCCCGGGCTCGAG	3122
Qy		1045	HisPheArgValTyrLeuSerLysGluAlaGluArgLysLeuLeuThrTrpGluSerVal	1064
Db		3123	CATTTCGGGTTTTACTTTCTAAGGAAGCGACGGAGCTGCTAACGTGGAAATCGGGTG	3182
Qy		1065	HisLysGluAsnPheLeuLeuAlaArgLeuAlaArgLysGluSerAspLeuArgLeu	1084
Db		3183	CATAAGGAAGACTTTCTGCTGSCACGCGCTAAGGCAAGCGGGAAGCGACTCCGAGCGT	3242
Qy		1085	LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu	1104
Db		3243	CTGGAGGCGCACTGCCAGAGGTGACATGSCACTGAAACAGCTGGACACATCCGGGAG	3302
Qy		1105	TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly	1124
Db		3303	TAGAACACGCGCTGAAGTGTCTGGAGCGGAGSTGCACAGTGTATGCGCGCTCTGGGG	3362
Qy		1125	TrpValThr 1127	
Db		3363	TGGGTGACG 3371	

